1 Data input and handling

Multiple sequence alignment (MSA)

Positions

	1	5		45	50

Sequences

1 IVGGYTCQ · · · CNYVDWIQ
2 IVGGR--R · · · AQFVNWID
3 IIGGH-AK · · · STFLSWIK
4 ITNGAYDG · · · TSQLNWIR
5 VNGNFDCG · · · GLYSGWIQ

Phylogenetic tree

NW
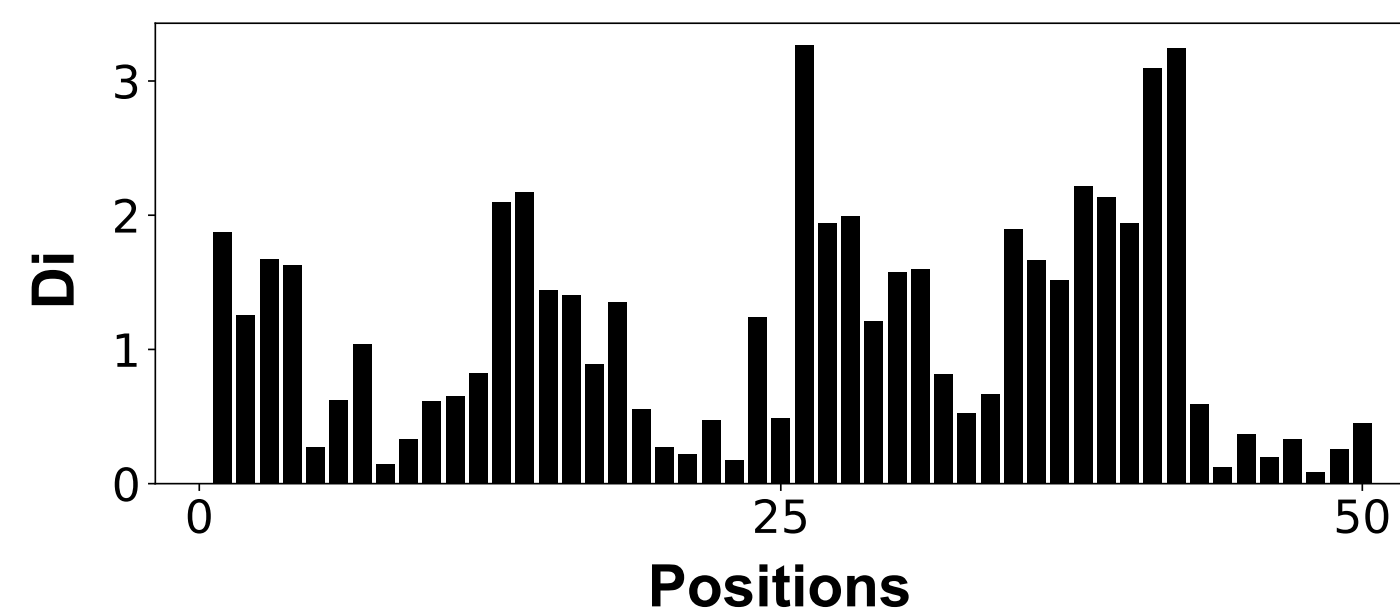
Metadata

CSV

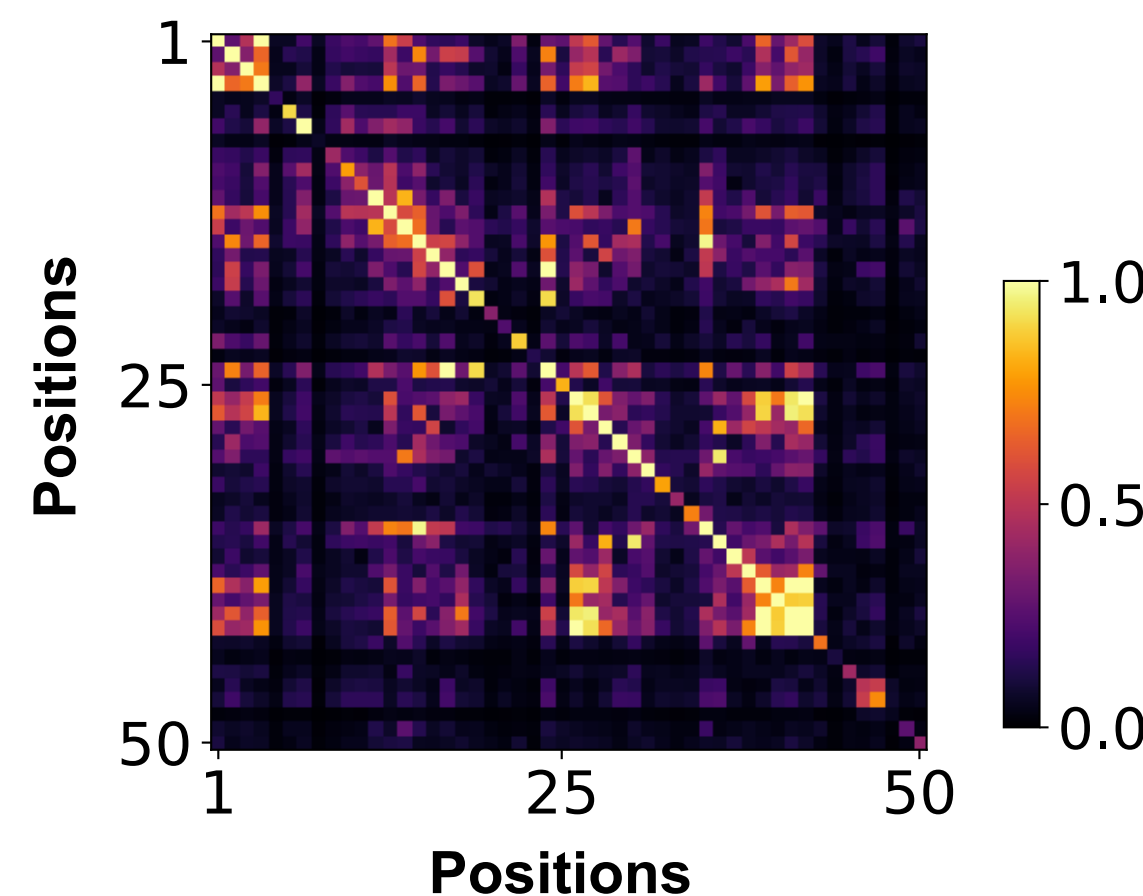**3D protein structure**

PDB

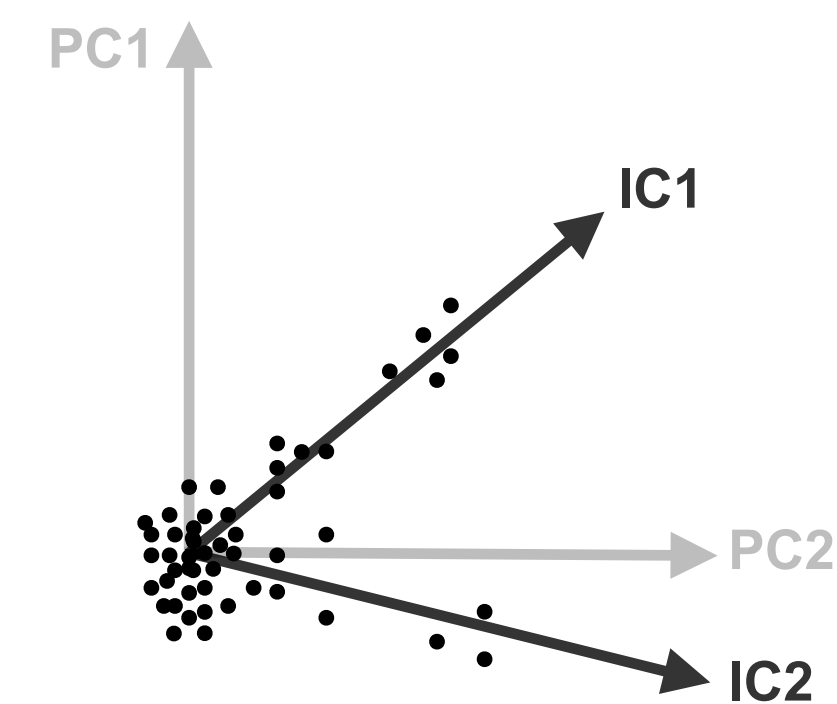# 2 Statistics and metrics
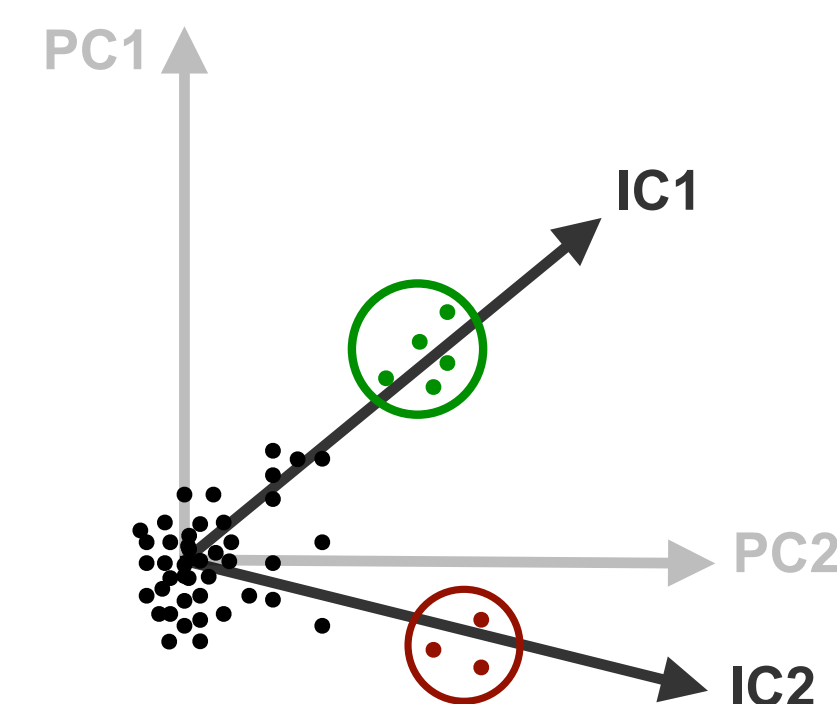
Conservation per position

Coevolution matrix

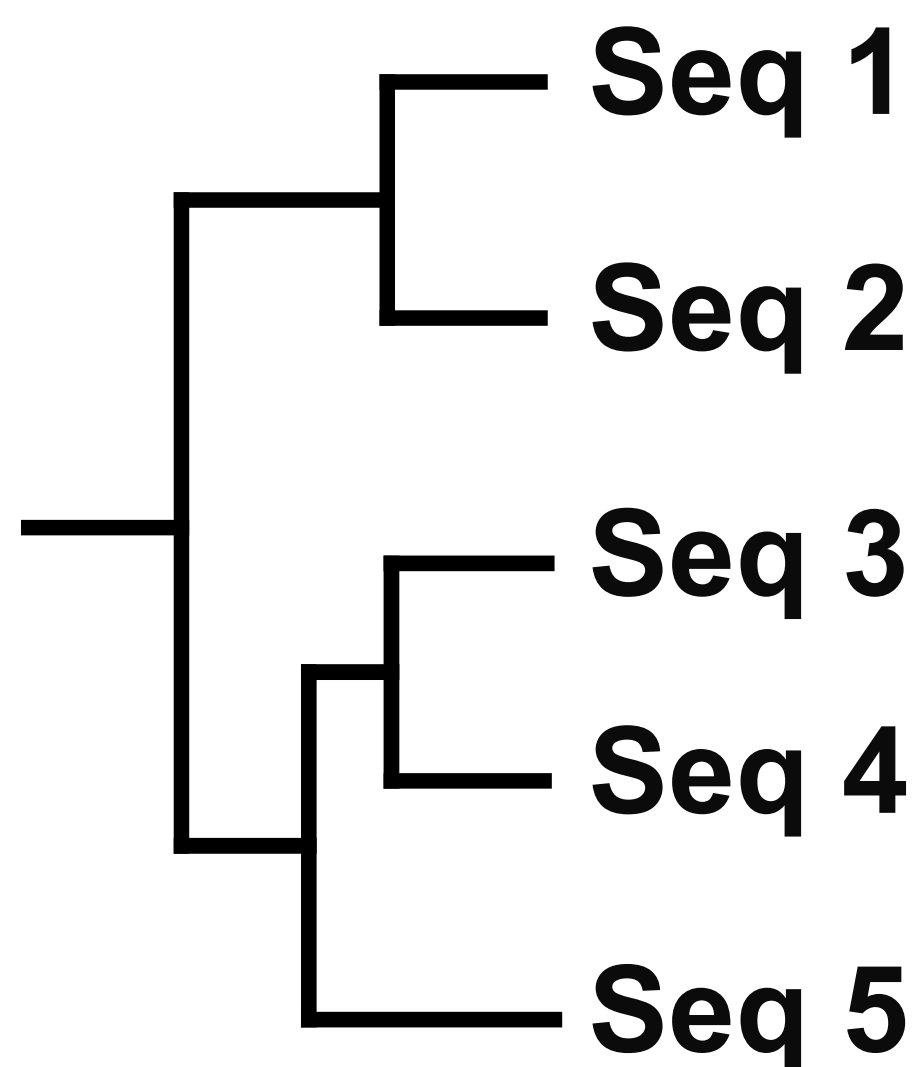
3 Deconvolution

Independant Component Analysis (ICA)

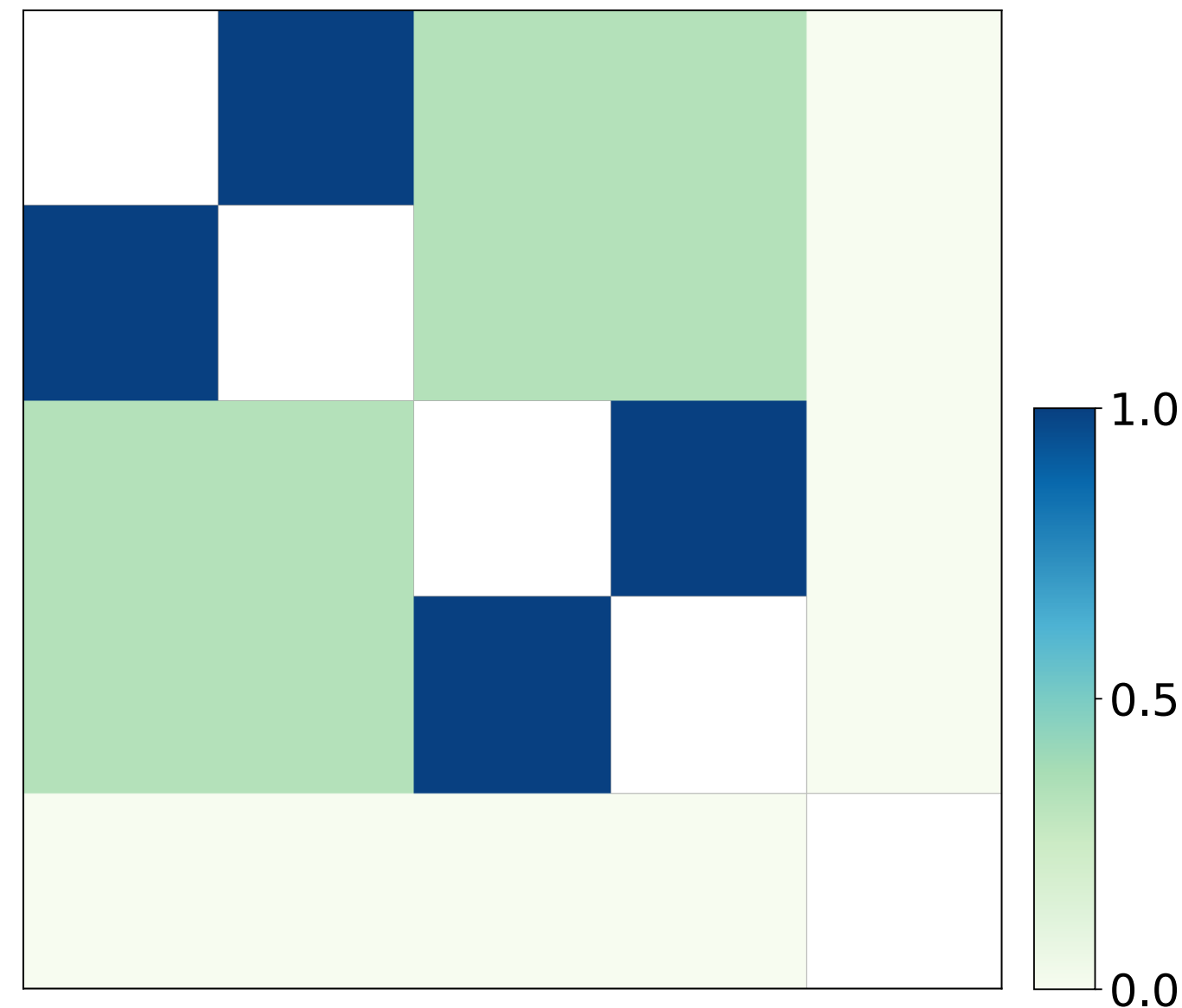## Extraction of sectors

4 Visualization

Phylogenetic tree

Sector sequence

Function

Sequence identity between sectors

Sector residues on 3D structure

Seq 1   V Q L
Seq 2   V Q L
Seq 3   N Q I
Seq 4   N Q I
Seq 5   G W P